IN THE CLAIMS

Please cancel claims 33-54 and add new claims 55-72.

1-54: (cancelled)

55. (new): A method of reconstituting a target protein from protein fragments in a plant, comprising:

(a) splitting a gene encoding a target protein into at least two DNA fragments;

(b) separating the DNA fragments of step (a) to prevent transmission of the gene to other plants; wherein one of the DNA fragments coding for a portion of the target protein is compartmentalized in the nucleus, and the other DNA fragment coding for another portion of the target protein is compartmentalized in the chloroplast;

(c) expressing the DNA fragments of step (b) within the plant to produce the corresponding fragments of the target protein; and

(d) reconstituting the target protein from the protein fragments in the plant.

56. (new): A method of preventing transmission to a second plant of a gene coding for a target protein in a first plant, comprising:

(a) splitting the gene encoding the target protein into at least two DNA fragments; and

(b) separating the DNA fragments of step (a) wherein one of the DNA fragments coding for a portion of the target protein is compartmentalized in the nucleus of a host cell in the first plant, and the other DNA fragment coding for another portion of the target protein is compartmentalized in the chloroplasts of the host cell; and

(c) preventing transmission of the gene coding for the target protein to the second plant .

57. (new): A method according to claim 55, wherein at least one of the DNA fragments is fused to a DNA sequence encoding a transit peptide for transport into a chloroplast or nucleus.

58. (new): The method of claim 55 or 56, wherein at least one of the DNA fragments is fused to a DNA coding for an intein or portions thereof.

59. (new) The method of claim 58, wherein one of the DNA fragments is formed by linking a 5' end of the DNA fragment coding for an N-terminal portion of the target protein to a 3' end of the DNA coding for an N-terminal portion of the intein, and another of the fusion fragments is formed by linking a 5' terminal end of DNA encoding a C-terminal portion of the target protein to the 3' end of DNA coding for a C-terminal portion of the intein.

60. (new): The method of claims 55 or 56 wherein the DNA coding for the target protein is split to form two or more DNA fragments by means of a DNA coding for one or more affinity domains.

61. (new): The method of claim 60, wherein the affinity domain is selected from the group consisting of inteins or intein fragments, leucine zipper and c-Jun/c-Fos.

62. (new): The method of claim 58, in which at least one of the DNA fragments coding for the target protein is fused to a DNA sequence encoding a transit peptide such that the protein product of the DNA fragment is transported into a single compartment where functional reconstitution can occur.

63. (new): The method of claim 58, wherein reconstitution of the target protein fragments comprises intein-mediated splicing.

64. (new): The method of claim 58, wherein reconstitution of the target protein fragments comprises intein-mediated protein complementation.

65. (new): The method of claim 55, wherein reconstitution of the target protein fragments comprises protein complementation.

66. (new): The method of claim 65, wherein protein complementation occurs in the presence of an affinity domain.

67. (new): The method of claim 65, wherein protein complementation occurs in the absence of an affinity domain.

68. (new): The method of claim 55 or 56, wherein splitting of the gene comprises:

(a) determining one or more potential split site regions of the target protein; and

(b) splitting the DNA coding for the target protein at the potential split site region.

69. (new): The method of claim 68, wherein the potential split site region of the target protein is determined by analyzing primary amino acid sequence of the target protein for non-conserved regions.

70. (new): The method of claim 68, wherein the potential split site region is determined by linker tolerance of linker insertion within the target protein.

71. (new): The method of claim 68, wherein the potential split site region is determined by analyzing the structure of the target protein for the presence of flexible loops.

72. (new): The method of claim 68, wherein the potential split site region is determined by analyzing the structure of the target protein

for the presence of amino acid sequence between folding domains of the target protein.